

PATENT
U.S.S.N. 10/054,611
Docket 002970US; 018/182c

CLAIM AMENDMENTS

1. *(Currently Amended)* A method of identifying a nucleic acid that encodes human telomerase reverse transcriptase (hTERT) or fragment thereof in a sample, comprising:
 - a) combining the sample with a polynucleotide probe such that the probe hybridizes specifically to the nucleic acid if the nucleic acid encodes hTERT or fragment thereof;
 - b) detecting any hybrid formed as a result of a); and
 - c) identifying the nucleic acid as encoding hTERT or fragment thereof if the hybrid is detected;wherein the probe hybridizes specifically to a DNA having the sequence of the hTERT encoding region of SEQ. ID NO:224 at 5°C to 25°C below T_m in aqueous solution at 1 M NaCl but does not hybridize to a DNA having the sequence of SEQ. ID NO:62 under the same reaction conditions;
wherein T_m is the melting temperature of double-stranded DNA having the sequence of said encoding region under the same reaction conditions.
2. *(Currently Amended)* A method of detecting a nucleic acid that encodes hTERT or fragment thereof in a sample, comprising:
 - a) combining the sample with a polynucleotide probe such that the probe hybridizes specifically to a nucleic acid comprising at least 100 consecutive nucleotides contained in SEQ. ID NO:224 if present in the sample;
 - b) detecting any hybrid formed as a result of a); and
 - c) identifying the nucleic acid as encoding hTERT or fragment thereof if the hybrid is detected;wherein the polynucleotide probe consists essentially of a sequence identical or complementary to 25 or more consecutive nucleotides from the hTERT encoding region of SEQ. ID NO:224 that are not contained in SEQ. ID NO:62.
3. *(Original)* The method of claim 2, wherein the hTERT nucleic acid is human genomic DNA.
4. *(Previously presented)* The method of claim 2, wherein the hTERT nucleic acid is mRNA or cDNA.
5. *(Previously presented)* The method of claim 2, wherein the hTERT nucleic acid consists essentially of 250 or more nucleotides of SEQ. ID NO:224.
6. *(Previously presented)* The method of claim 2, wherein the hTERT nucleic acid consists essentially of 500 or more nucleotides of SEQ. ID NO:224.

PATENT
USSN 10/054,611
Docket 002970US; 018/182c

7. *(Previously presented)* The method of claim 2, wherein the probe consists essentially of a sequence identical or complementary to 30 or more consecutive nucleotides from the hTERT encoding region of SEQ. ID NO:224.
8. *(Previously presented)* The method of claim 2, wherein the probe consists essentially of a sequence identical or complementary to 50 or more consecutive nucleotides from the hTERT encoding region of SEQ. ID NO:224.
9. *(Previously presented)* The method of claim 2, wherein the probe consists essentially of a sequence identical or complementary to 100 or more consecutive nucleotides from the hTERT encoding region of SEQ. ID NO:224.

10 to 12. CANCELLED

13. *(Currently Amended)* A method of identifying a nucleic acid that encodes hTERT or fragment thereof in a sample, comprising:
 - a) combining the sample with a polynucleotide primer under conditions that the primer specifically primes amplification of SEQ. ID NO:224 or fragment thereof if present in the sample;
 - b) detecting any amplification product formed as a result of a); and
 - c) identifying the nucleic acid as encoding hTERT or fragment thereof if the amplification product is detected;wherein the primer hybridizes specifically to a DNA having the sequence of the hTERT encoding region of SEQ. ID NO:224 at 5°C to 25°C below T_m in aqueous solution at 1 M NaCl but does not hybridize to a DNA having the sequence of SEQ. ID NO:62 under the same reaction conditions;
wherein T_m is the melting temperature of double-stranded DNA having the sequence of said encoding region under the same reaction conditions.
14. *(Currently Amended)* A method of detecting a nucleic acid encoding hTERT or fragment thereof in a sample, comprising:
 - a) combining the sample with polynucleotide primers so as to prime amplification of nucleic acid encoding hTERT or fragment thereof if present in the sample;
 - b) detecting any amplified product formed as a result of a); and
 - c) identifying the nucleic acid as encoding hTERT or fragment thereof if the amplification product is detected;wherein each of said primers consists essentially of a sequence identical or complementary to 15 or more consecutive nucleotides from the hTERT encoding region of SEQ. ID NO:224 but

PATENT
USSN 10/054,611
Docket 002970US; 018/182c

at least one of the primers does not consist of a sequence identical or complementary to 15 or more consecutive nucleotides from SEQ. ID NO:62.

15. *(Previously presented)* The method of claim 14, wherein each of said primers consists essentially of a sequence identical or complementary to 30 or more consecutive nucleotides from the hTERT encoding region of SEQ. ID NO:224.
16. *(Previously presented)* The method of claim 14, wherein each of said primers consists essentially of a sequence identical or complementary to 50 or more consecutive nucleotides from the hTERT encoding region of SEQ. ID NO:224.

17 to 22. CANCELLED

23. *(Withdrawn)* ~~A combination~~ A pair of oligonucleotide primers for PCR amplification for use in detecting an hTERT nucleic acid according to claim 14, wherein each primer consists essentially of a sequence identical or complementary to 15 or more consecutive nucleotides from the hTERT encoding region of SEQ. ID NO:224 but at least one of the primers does not consist of a sequence identical or complementary to 15 or more consecutive nucleotides from SEQ. ID NO:62.

24 to 25. CANCELLED

26 to 34. CANCELLED

35. *(Previously presented)* The method of claim 1, wherein a) comprises combining the sample with the probe at 5°C to 25°C below T_m in aqueous solution at 1 M NaCl.
36. CANCELLED
37. *(Previously presented)* The method of claim 1, wherein the probe comprises a sequence identical or complementary to 100 or more consecutive nucleotides from the hTERT encoding region of SEQ. ID NO:224.
38. CANCELLED.
39. *(Previously presented)* The method of claim 1, wherein the sample has been taken from a patient having a tumor.

PATENT
USSN 10/054,611
Docket 002970US; 018/182c

40. *(Previously presented)* The method of claim 2, wherein the sample has been taken from a patient having a tumor.
41. *(Previously presented)* The method of claim 13, wherein a) comprises combining the sample with the primer at 5°C to 25°C below T_m in aqueous solution at 1 M NaCl.
42. *CANCELLED.*
43. *(Previously presented)* The method of claim 13, wherein the primer comprises a sequence identical or complementary to 30 or more consecutive nucleotides from the hTERT encoding region of SEQ. ID NO:224.
44. *CANCELLED*
45. *(Previously presented)* The method of claim 13, wherein the sample has been taken from a patient having a tumor.
46. *(Previously presented)* The method of claim 14, wherein the sample has been taken from a patient having a tumor.

PATENT
USSN 10/054,611
Docket 002970US; 018/182c

47. (New) A method of identifying a nucleic acid that encodes human telomerase reverse transcriptase (hTERT) or fragment thereof in a sample, comprising:
- a) combining the sample with a polynucleotide probe such that the probe hybridizes specifically to the nucleic acid if the nucleic acid encodes hTERT or fragment thereof;
 - b) detecting any hybrid formed as a result of a); and
 - c) identifying the nucleic acid as encoding hTERT or fragment thereof if the hybrid is detected;
- wherein the probe hybridizes specifically to a DNA having a sequence consisting of SEQ. ID NO:62 at 5°C to 25°C below T_m in aqueous solution at 1 M NaCl;
- wherein T_m is the melting temperature of double-stranded DNA having the sequence of SEQ. ID NO:62 under the same reaction conditions.
48. (New) The method of claim 47, wherein a) comprises combining the sample with the probe at 5°C to 25°C below T_m in aqueous solution at 1 M NaCl.
49. (New) The method of claim 47, wherein the probe comprises a sequence identical or complementary to 100 or more consecutive nucleotides from SEQ. ID NO:62.
50. (New) The method of claim 47, wherein the probe is a fragment of SEQ. ID NO:62.
51. (New) The method of claim 47, wherein the sample has been taken from a patient having a tumor.
52. (New) A method of detecting a nucleic acid that encodes hTERT or fragment thereof in a sample, comprising:
- a) combining the sample with a polynucleotide probe such that the probe hybridizes specifically to a nucleic acid comprising at least 100 consecutive nucleotides contained in SEQ. ID NO:62 if present in the sample;
 - b) detecting any hybrid formed as a result of a); and
 - c) identifying the nucleic acid as encoding hTERT or fragment thereof if the hybrid is detected;
- wherein the polynucleotide probe consists essentially of a sequence identical or complementary to 25 or more consecutive nucleotides from SEQ. ID NO:62.
53. (New) The method of claim 52, wherein the probe consists essentially of a sequence identical or complementary to 30 or more consecutive nucleotides from SEQ. ID NO:62.

Best Available Copy

PATENT
USSN 10/054,611
Docket 002970US; 018/182c

54. (New) The method of claim 52, wherein the probe consists essentially of a sequence identical or complementary to 50 or more consecutive nucleotides from SEQ. ID NO:62.
55. (New) The method of claim 52, wherein the probe consists essentially of a sequence identical or complementary to 100 or more consecutive nucleotides from SEQ. ID NO:62.
56. (New) The method of claim 52, wherein the sample has been taken from a patient having a tumor.
57. (New) A method of identifying a nucleic acid that encodes hTERT or fragment thereof in a sample, comprising:
- a) combining the sample with a polynucleotide primer under conditions that the primer specifically primes amplification of SEQ. ID NO:62 or fragment thereof if present in the sample;
 - b) detecting any amplification product formed as a result of a); and
 - c) identifying the nucleic acid as encoding hTERT or fragment thereof if the amplification product is detected;
- wherein the primer hybridizes specifically to a DNA having a sequence consisting of SEQ. ID NO:62 at 5°C to 25°C below T_m in aqueous solution at 1 M NaCl;
- wherein T_m is the melting temperature of double-stranded DNA having the sequence of SEQ. ID NO:62 under the same reaction conditions.
58. (New) The method of claim 57, wherein a) comprises combining the sample with the primer at 5°C to 25°C below T_m in aqueous solution at 1 M NaCl.
59. (New) The method of claim 57, wherein the primer comprises a sequence identical or complementary to 30 or more consecutive nucleotides from SEQ. ID NO:62.
60. (New) The method of claim 57, wherein the probe is a fragment of SEQ. ID NO:62.
61. (New) The method of claim 57, wherein the sample has been taken from a patient having a tumor.

PATENT
USSN 10/054,611
Docket 002970US; 018/182c

62. (New) A method of detecting a nucleic acid encoding hTERT or fragment thereof in a sample, comprising:
- a) combining the sample with polynucleotide primers so as to prime amplification of nucleic acid encoding hTERT or fragment thereof if present in the sample;
 - b) detecting any amplified product formed as a result of a); and
 - c) identifying the nucleic acid as encoding hTERT or fragment thereof if the amplification product is detected;
- wherein each of said primers consists essentially of a sequence identical or complementary to 15 or more consecutive nucleotides from SEQ. ID NO:62.
63. (New) The method of claim 62, wherein each of said primers consists essentially of a sequence identical or complementary to 30 or more consecutive nucleotides from SEQ. ID NO:62.
64. (New) The method of claim 62, wherein each of said primers consists essentially of a sequence identical or complementary to 50 or more consecutive nucleotides from SEQ. ID NO:62.
65. (New) A pair of oligonucleotide primers for PCR amplification for use in detecting an hTERT nucleic acid according to claim 62, wherein each primer consists essentially of a sequence identical or complementary to 15 or more consecutive nucleotides from SEQ. ID NO:62.
66. (New) The method of claim 62, wherein the sample has been taken from a patient having a tumor.